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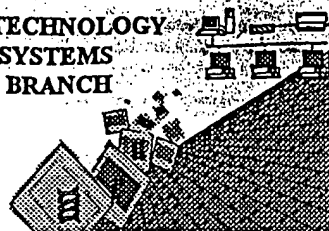
**ATTACHMENT TO "NOTICE TO COMPLY WITH  
REQUIREMENTS...SEQUENCE DISCLOSURES"**

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be submitted using one of the following methods:

1. Electronically submitted through EFS-Bio  
(<http://www.uspto.gov/ebs/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
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## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/083,842  
Source: OIP  
Date Processed by STIC: 3/19/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
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U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

01PE

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/083,842

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ✓ Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

**Does Not Comply  
Corrected Diskette Needed**

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/083,842

DATE: 03/19/2002  
TIME: 16:15:26

Input Set : A:\EP.txt  
Output Set: N:\CRF3\03192002\J083842.raw

→ The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

3 <110> APPLICANT: Syngenta Biotechnology, Inc.  
4 Grina, Jonas  
6 <120> TITLE OF INVENTION: NOVEL CYANOENAMINES USEFUL AS LIGANDS FOR MODULATING GENE  
EXPRESSION IN  
7 PLANTS OR ANIMALS  
9 <130> FILE REFERENCE: 1392/2/2  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/083,842  
C--> 11 <141> CURRENT FILING DATE: 2002-02-27  
11 <150> PRIOR APPLICATION NUMBER: 60/272,905  
12 <151> PRIOR FILING DATE: 2001-03-02  
14 <160> NUMBER OF SEQ ID NOS: 12  
16 <170> SOFTWARE: PatentIn version 3.1  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 17  
20 <212> TYPE: DNA  
21 <213> ORGANISM: synthetic construct  
23 <400> SEQUENCE: 1  
24 agcttgaggg tataatg 17  
27 <210> SEQ ID NO: 2  
28 <211> LENGTH: 17  
29 <212> TYPE: DNA  
30 <213> ORGANISM: synthetic construct  
32 <400> SEQUENCE: 2  
33 actcccatat tactga 17  
36 <210> SEQ ID NO: 3  
37 <211> LENGTH: 36  
38 <212> TYPE: DNA  
39 <213> ORGANISM: synthetic construct  
41 <400> SEQUENCE: 3  
42 gatccgagac aagggttcaa tgcacttgct caatga 36  
45 <210> SEQ ID NO: 4  
46 <211> LENGTH: 36  
47 <212> TYPE: DNA  
48 <213> ORGANISM: synthetic construct  
50 <400> SEQUENCE: 4  
51 gctctgttcc caagttacgt gaacaggta ctctag 36  
54 <210> SEQ ID NO: 5  
55 <211> LENGTH: 147  
56 <212> TYPE: DNA  
57 <213> ORGANISM: synthetic construct  
59 <400> SEQUENCE: 5  
60 gatccgagac aagggttcaa tgcacttgct caatgagatc cgagacaagg gttcaatgca 60  
62 cttgtccaat gagatctcat tggacaagtg cattgaacct tgtctcggat ctcatggac 120  
64 aagtgcattg aacccttgct tcggatc 147

invalid response, see error summary sheet, item 10  
4-11



RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/083,842

DATE: 03/19/2002

TIME: 16:15:26

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J083842.raw

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67 <210> SEQ ID NO: 6
68 <211> LENGTH: 2840
69 <212> TYPE: DNA
70 <213> ORGANISM: Manduca sexta
72 <220> FEATURE:
73 <221> NAME/KEY: CDS
74 <222> LOCATION: (361)..(2031)
75 <223> OTHER INFORMATION:
78 <400> SEQUENCE: 6
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81 aacctccgtc tccacatcac cgagcgaact ctagaactcg cgtactcttc tcacctgttg      120
83 cttcggattg tggtgtgact gaaaagcgac gcgtatcgtg gtcgaagatt ctctataagt      180
85 gcataatata ttcgagacag tggatagcga ttcgtttcgg ttcatcgcg cggtatgagt      240
87 gttcatgccc gtagagacgc gtttagatag ttatggcgag gaaaaagtga agtgaaaagcc      300
89 tacgtcagag gatgtccctc ggtggtcacg gaagccgggg cgtgtgacgc gctcttcgac      360
91 atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt      408
92 Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe
93 1          5          10          15
95 gag gag agc tcc tct gaa gtg act tct tcc tcg gcg ttc ggg atg ccg      456
96 Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Ala Phe Gly Met Pro
97          20          25          30
99 gcg gcc atg gta atg tca ccg gag tcg ctg gcg tcg cca gag tac ggc      504
100 Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
101          35          40          45
103 ggc ctc gag ctc tgg agc tac gat gag acc atg aca aac tat ccg gcg      552
104 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
105          50          55          60
107 cag tca ctg ctc ggc gcg tgt aat gcg ccg cag cag cag cag caa cag      600
108 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln Gln
109 65          70          75          80
111 caa caa cag cag ccg tcc gct cag ccg ctg ccg tct atg ccg ctg ccg      648
112 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
113          85          90          95
115 atg cct cct aca act cct aaa tca gag aac gag tcc atg tcg tca ggt      696
116 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
117          100          105          110
119 cga gaa gaa tta tca ccg gcc tca agt ata aat gga tgt agt act gat      744
120 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
121          115          120          125
123 ggg gaa cca aga cga cag aag aaa ggg cca gcg ccg cgc cag cag gag      792
124 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
125          130          135          140
127 gaa ctg tgc ctt gtt tgc ggc gac agg gct tcg gga tat cac tat aac      840
128 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
129 145          150          155          160
131 gcg ctt acg tgc gaa gga tgt aaa ggg ttc ttc agg cgg agt gtg acc      888
132 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
133          165          170          175
135 aag aat gcg gta tat att tgt aaa ttt gga cac gcc tgc gag atg gac      936

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DATE: 03/19/2002

TIME: 16:15:26

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J083842.raw

136	Lys	Asn	Ala	Val	Tyr	Ile	Cys	Lys	Phe	Gly	His	Ala	Cys	Glu	Met	Asp	
137				180					185					190			
139	atg	tac	atg	agg	aga	aaa	tgc	caa	gag	tgt	cgg	ttg	aag	aaa	tgc	ctc	984
140	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	
141			195				200					205					
143	gcg	gtg	ggc	atg	agg	ccc	gag	tgc	gtc	gtc	cca	gag	tcc	acg	tgc	aag	1032
144	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Ser	Thr	Cys	Lys	
145		210					215					220					
147	aac	aaa	aga	aga	gaa	aag	gaa	gca	cag	aga	gaa	aaa	gac	aaa	ctg	cca	1080
148	Asn	Lys	Arg	Arg	Glu	Lys	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Leu	Pro	
149	225					230					235				240		
151	gtc	agt	acg	acg	aca	gtg	gac	gat	cat	atg	cct	gcc	ata	atg	caa	tgt	1128
152	Val	Ser	Thr	Thr	Thr	Val	Asp	Asp	His	Met	Pro	Ala	Ile	Met	Gln	Cys	
153				245						250					255		
155	gac	cct	ccg	ccc	cca	gag	gcg	gca	agg	att	cac	gaa	gtg	gtc	ccg	agg	1176
156	Asp	Pro	Pro	Pro	Glu	Ala	Ala	Arg	Ile	His	Glu	Val	Val	Pro	Arg		
157			260					265					270				
159	ttc	cta	acg	gag	aag	cta	atg	gag	cag	aac	aga	ctg	aag	aat	gtg	acg	1224
160	Phe	Leu	Thr	Glu	Lys	Leu	Met	Glu	Gln	Asn	Arg	Leu	Lys	Asn	Val	Thr	
161			275				280					285					
163	ccg	ctg	tcg	gcg	aac	cag	aag	tcc	ctg	atc	gcg	agg	ctc	gtg	tgg	tac	1272
164	Pro	Leu	Ser	Ala	Asn	Gln	Lys	Ser	Leu	Ile	Ala	Arg	Leu	Val	Trp	Tyr	
165		290				295					300						
167	cag	gag	ggg	tac	gag	cag	ccg	tcg	gag	gaa	gat	ctc	aag	aga	gtt	aca	1320
168	Gln	Glu	Gly	Tyr	Glu	Gln	Pro	Ser	Glu	Glu	Asp	Leu	Lys	Arg	Val	Thr	
169	305				310					315					320		
171	cag	aca	tgg	cag	tta	gaa	gaa	gaa	gaa	gag	gag	gaa	act	gac	atg	ccc	1368
172	Gln	Thr	Trp	Gln	Leu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Thr	Asp	Met	Pro	
173				325						330					335		
175	ttc	cgt	cag	atc	aca	gag	atg	acg	atc	tta	aca	gtg	cag	ctt	att	gta	1416
176	Phe	Arg	Gln	Ile	Thr	Glu	Met	Thr	Ile	Leu	Thr	Val	Gln	Leu	Ile	Val	
177			340					345					350				
179	gaa	ttc	gca	aag	gga	cta	ccg	gga	ttc	tcc	aag	ata	tct	cag	tcc	gat	1464
180	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Gly	Phe	Ser	Lys	Ile	Ser	Gln	Ser	Asp	
181		355				360					365						
183	caa	att	aca	tta	tta	aag	gcg	tca	tca	agc	gaa	gtg	atg	atg	ctg	cga	1512
184	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Ser	Ser	Ser	Glu	Val	Met	Met	Leu	Arg	
185		370				375					380						
187	gtg	gcg	cga	cgg	tac	gac	gcg	gcg	acg	gac	agc	gtg	ctg	ttc	gcg	aac	1560
188	Val	Ala	Arg	Arg	Tyr	Asp	Ala	Ala	Thr	Asp	Ser	Val	Leu	Phe	Ala	Asn	
189	385				390					395					400		
191	aac	cag	gcg	tac	acg	cgc	gac	aac	tac	cgc	aag	gcg	ggc	atg	tcc	tac	1608
192	Asn	Gln	Ala	Tyr	Thr	Arg	Asp	Asn	Tyr	Arg	Lys	Ala	Gly	Met	Ser	Tyr	
193				405					410					415			
195	gtc	atc	gag	gac	ctg	ctg	cac	ttc	tgt	cgg	tgt	atg	tac	tcc	atg	agc	1656
196	Val	Ile	Glu	Asp	Leu	Leu	His	Phe	Cys	Arg	Cys	Met	Tyr	Ser	Met	Ser	
197			420					425					430				
199	atg	gac	aat	gtg	cac	tac	gcg	ctg	ctc	acc	gcc	atc	gtt	ata	ttc	tca	1704
200	Met	Asp	Asn	Val	His	Tyr	Ala	Leu	Leu	Thr	Ala	Ile	Val	Ile	Phe	Ser	

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Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J083842.raw

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203 gac cgg cca ggc ctc gag caa ccc ctt tta gtg gag gaa atc cag aga      1752
204 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg
205          450          455          460
207 tac tac ttg aag acg ctg cgg gtt tac att tta aat cag cac agc gcg      1800
208 Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala
209 465          470          475          480
211 tcg cct cgc tgc gcc gtg ctg ttc ggc aag atc ctc ggc gtg ctg acg      1848
212 Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr
213          485          490          495
215 gaa ctg cgc acg ctc ggc acg cag aac tcc aac atg tgc atc tcg ctg      1896
216 Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu
217          500          505          510
219 aag ctg aag aac agg aaa ctt ccg cca ttc ctc gag gag atc tgg gac      1944
220 Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp
221          515          520          525
223 gtg gcc gaa gtg tcg acg acg cag ccg acg ccg ggg gtg gcg gcg cag      1992
224 Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln
225          530          535          540
227 gtg acc ccc atc gtg gtg gac aac ccc gcg gcg ctc tag ctggcgcgcc      2041
228 Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu
229 545          550          555
231 ggcgcgcgcg cccgcgcgcc ccgcccgcgc cgctcccccg cgccgcgcgc gcgcgcgcgc      2101
233 gcggcctgcg ctgagtgccg gacccgcgcc gagagagaaa cgctcataga ctggctagtt      2161
235 ttagtgaagt gcacggacgc gatcgtggga ccgcatcgac gcgtccgtga ggacagtga      2221
237 aatattaccg ctagggccgg ttctgacgtg tccggtgacc gacgacgatg atgcgcgtga      2281
239 gattagtga tatatgtgtt gttgaacgtt tggagagtat atttagtggt gatcgtcggg      2341
241 agcgcgcgcg cggcgcgtgt cggcgagctg tccgcgcgcg gccgcgcgcg gcgactccgc      2401
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245 cttcttttcga taaataagtt caccgtgtatt gcgcgtacat acgagaatta taaagaaaaa      2521
247 aagtaataata tgaagagatg tttctatttg gtgaaaagtt taaacttatg tttatttacc      2581
249 aaaataaact atacgttgat cgaccttttg actataatat tgtgctgggt cgttggcagc      2641
251 ggcgcgacgaa cgcgcgcgca ccatatttgt ttatatatag tttatgtgag acgttatcgt      2701
253 gtctgttcca cttagttccg attcatgttc caccaggtcg gtgtagtgat cagggcgggc      2761
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261 <211> LENGTH: 556
262 <212> TYPE: PRT
263 <213> ORGANISM: Manduca sexta
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272          20          25          30
275 Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
276          35          40          45
279 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
280          50          55          60

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Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J083842.raw

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287 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
288 85 90 95
291 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
292 100 105 110
295 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
296 115 120 125
299 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
300 130 135 140
303 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
304 145 150 155 160
307 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
308 165 170 175
311 Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
312 180 185 190
315 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
316 195 200 205
319 Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys
320 210 215 220
323 Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro
324 225 230 235 240
327 Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys
328 245 250 255
331 Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg
332 260 265 270
335 Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr
336 275 280 285
339 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr
340 290 295 300
343 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr
344 305 310 315 320
347 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro
348 325 330 335
351 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val
352 340 345 350
355 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
356 355 360 365
359 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
360 370 375 380
363 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
364 385 390 395 400
367 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
368 405 410 415
371 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser
372 420 425 430
375 Met Asp Asn Val His Tyr Ala Leu Thr Ala Ile Val Ile Phe Ser
376 435 440 445
379 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg

```



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/083,842

DATE: 03/19/2002

TIME: 16:15:28

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J083842.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date